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SEQUENCE LISTING

<110> Lye, Stephen
Dong, Xuesen
<120> METHODS AND COMPOSITIONS FOR MODULATING A STEROID RECEPTOR
<130> MTS6USA
<140> PCT/CA2005/000042
<141> 2005-01-14
<150> 60/536,598
<151> 2004-01-15
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Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
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Pro His Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
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Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
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Gln Gln Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
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Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser
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Ser Ser Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly
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Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Pro Ala Val Thr Ser Ala
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Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
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Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro
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Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
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Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
210 215 220

Ser Thr Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu
225 230 235 240

Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
245 250 255

Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
260 265 270

Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
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Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
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Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
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Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
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Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
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Glu Gly Val Phe Leu Leu Thr Thr Pro Arg Pro Val Ile Val Glu
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Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
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Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Pro Arg Phe
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Lys Asp Ala Lys Asp Lys Leu Glu Ser Glu Met Glu Asp Ala Tyr His
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Glu Leu Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg
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Lys Glu Met Gln Leu Arg Gln Glu Glu Glu Arg Arg Arg Arg Glu Glu
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Glu Met Met Ile Arg Gln Arg Glu Met Glu Glu Gln Met Arg Arg Gln
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Asp Met Arg Met Gly Gly Gly Ala Met Asn Met Gly Asp Pro Tyr
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Pro Arg Phe
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Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
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Pro His Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
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Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
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Gln Gln Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
100 105 110

Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Thr Pro Pro Ala Ser
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145 150 155 160

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165 170 175

Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro
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Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
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Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
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Ser Thr Pro Gly Gly His Pro Lys Pro Pro Arg Arg Gly Gly Glu
225 230 235 240

Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
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Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
260 265 270

Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
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Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
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Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
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Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
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Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
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Glu Leu Leu Glu Glu Ala Phe Ser Gln Phe Gly Pro Ile Glu Arg Ala
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Val Val Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val
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Glu Phe Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser
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Glu Gly Val Phe Leu Leu Thr Thr Pro Arg Pro Val Ile Val Glu
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Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
450 455 460

Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Thr Arg Phe
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Ala Gln His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser
485 490 495

Leu Asp Glu Met Glu Lys Gln Gln Arg Glu Gln Val Glu Lys Asn Met
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Lys Asp Ala Lys Asp Lys Leu Glu Ser Glu Met Glu Asp Ala Tyr His
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Glu His Gln Ala Asn Leu Leu Arg Gln Asp Leu Met Arg Arg Gln Glu
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Glu Leu Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg
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Lys Glu Met Gln Leu Arg Gln Glu Glu Glu Arg Arg Arg Arg Glu Glu
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Glu Met Met Ile Arg Gln Arg Glu Met Glu Asp Gln Met Arg Arg Gln
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595 600 605

Asp Met Arg Met Gly Gly Gly Ala Met Asn Met Gly Asp Pro Tyr
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Gly Ser Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Ile

625

630

635

640

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Pro Arg Phe
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Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
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Pro His Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
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Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
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Gln Gln Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
100 105 110

Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser
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Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
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Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro
180 185 190

Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
195 200 205

Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
210 215 220

Ser Thr Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu
225 230 235 240

Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
245 250 255

Gln Gly Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
260 265 270

Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
275 280 285

Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu
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Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
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Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
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Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
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Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr
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His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
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Glu Leu Leu Glu Glu Ala Phe Ser Gln Phe Gly Pro Ile Glu Arg Ala
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Glu Phe Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser
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Glu Gly Val Phe Leu Leu Thr Thr Pro Arg Pro Val Ile Val Glu
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Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
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Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Pro Arg Phe
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Ala Gln His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser
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Leu Asp Glu Met Glu Lys Gln Gln Arg Glu Gln Val Glu Lys Asn Met
500 505 510

Lys Asp Ala Lys Asp Lys Leu Glu Ser Glu Met Glu Asp Ala Tyr His
515 520 525

Glu His Gln Ala Asn Leu Leu Arg Gln Asp Leu Met Arg Arg Gln Glu
530 535 540

Glu Leu Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg
545 550 555 560

Lys Glu Met Gln Leu Arg Gln Glu Glu Glu Arg Arg Arg Arg Glu Glu
565 570 575

Glu Met Met Ile Arg Gln Arg Glu Met Glu Glu Gln Met Arg Arg Gln
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Arg Glu Glu Ser Tyr Ser Arg Met Gly Tyr Met Asp Pro Arg Glu Arg
595 600 605

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610 615 620

Gly Ser Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Ile
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35 40 45

Gly Ser Ala Pro Pro Ala Ser Ser Ser Ala Pro Pro Ala Thr Pro Pro
50 55 60

Thr Ser Gly Ala Pro Pro Gly Ser Gly Pro Gly Pro Thr Pro Thr Pro
65 70 75 80

Pro Pro Ala Val Thr Ser Ala Pro Pro Gly Ala Pro Pro Pro Thr Pro
85 90 95

Pro Ser Ser Gly Val Pro Thr Thr Pro Pro Gln Ala Gly Gly Pro Pro
100 105 110

Pro Pro Pro Ala Ala Val Pro Gly Pro Gly Pro Gly Pro Lys Gln Gly
115 120 125

Pro Gly Pro Gly Gly Pro Lys Gly Gly Lys Met Pro Gly Gly Pro Lys
130 135 140

Pro Gly Gly Gly Pro Gly Leu Ser Thr Pro Gly Gly His Pro Lys Pro
145 150 155 160

Pro His Arg Gly Gly Glu Pro Arg Gly Gly Arg Gln His His Pro
165 170 175

Pro Tyr His Gln Gln His His Gln Gly Pro Pro Pro Gly Gly Pro Gly
180 185 190

Gly Arg Ser Glu Glu Lys Ile Ser Asp Ser Glu Gly Phe Lys Ala Asn
195 200 205

Leu Ser Leu Leu Arg Arg Pro Gly Glu Lys Thr Tyr Thr Gln Arg Cys
210 215 220

Arg Leu Phe Val Gly Asn Leu Pro Ala Asp Ile Thr Glu Asp Glu Phe
225 230 235 240

Lys Arg Leu Phe Ala Lys Tyr Gly Glu Pro Gly Glu Val Phe Ile Asn
245 250 255

Lys Gly Lys Gly Phe Gly Phe Ile Lys Leu Glu Ser Arg Ala Leu Ala
260 265 270

Glu Ile Ala Lys Ala Glu Leu Asp Asp Thr Pro Met Arg Gly Arg Gln
275 280 285

Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val Arg Asn
290 295 300

Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser Gln
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Phe Gly Pro Ile Glu Arg Ala val val Ile val Asp Asp Arg Gly Arg
325 330 335

Ser Thr Gly Lys Gly Ile val Glu Phe Ala Ser Lys Pro Ala Ala Arg
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Lys Ala Phe Glu Arg Cys Ser Glu Gly val Phe Leu Leu Thr Thr Thr
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370 375 380

Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln Lys Glu
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Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu Tyr Glu
405 410 415

Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln Gln Arg
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Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu Glu Ser
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Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu Arg Gln
450 455 460

Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu His
465 470 475 480

Asn Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln Glu Glu
485 490 495

Glu Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg Glu Met
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Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg Met Gly
515 520 525

Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly Ala
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Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe Pro Pro
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565 570 575

Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg Thr Glu
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Arg Phe Gly Gln Gly Gly Ala Gly Pro Val Gly Gly Gln Gly Pro Arg
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Pro Gly Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro
50 55 60

Pro His Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln
65 70 75 80

Gln Pro Pro Pro His Gln Pro Pro Pro His Pro Gln Pro His Gln Gln
85 90 95

Gln Gln Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala
100 105 110

Gln Gly Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser
115 120 125

Ser Ser Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly
130 135 140

Ser Gly Pro Gly Pro Thr Pro Thr Pro Pro Pro Ala Val Thr Ser Ala
145 150 155 160

Pro Pro Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr
165 170 175

Thr Pro Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro
180 185 190

Gly Pro Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys
195 200 205

Gly Gly Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Gly Pro Gly Leu
210 215 220

Ser Thr Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Gly Glu
225 230 235 240

Pro Arg Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His
245 250 255

Gln Gly Pro Pro Pro Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile
260 265 270

Ser Asp Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro
275 280 285

Gly Glu Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu

290 295 300
Pro Ala Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr
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Gly Glu Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe
325 330 335

Ile Lys Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu
340 345 350

Asp Asp Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr
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His Ala Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn
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385 390 395 400

Val Val Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val
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Glu Phe Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser
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Glu Gly Val Phe Leu Leu Thr Thr Pro Arg Pro Val Ile Val Glu
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Pro Leu Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala
450 455 460

Gln Lys Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Pro Arg Phe
465 470 475 480

Ala Gln His Gly Thr Phe Glu Tyr Glu Tyr Ser Gln Arg Trp Lys Ser
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Arg Asn Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe
65 70 75 80

Ser Gln Phe Gly Pro Ile Glu Arg Ala Val Val Ile Val Asp Asp Arg
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Gly Arg Ser Thr Gly Lys Gly Ile Val Glu Phe Ala Ser Lys Pro Ala
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Ala Arg Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr
115 120 125

Thr Thr Pro Arg Pro Val Ile Val Glu Pro Leu Glu Gln Leu Asp Asp
130 135 140

Glu Asp Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln
145 150 155 160

Lys Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu
165 170 175

Tyr Glu Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln
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Gln Arg Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu
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Glu Ser Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu
210 215 220

Arg Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu
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Leu His Asn Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln
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Glu Glu Glu Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg
260 265 270

Glu Met Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg
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Met Gly Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly
290 295 300

Gly Ala Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe
305 310 315 320

Pro Pro Leu Gly Gly Gly Ile Gly Tyr Glu Ala Asn Pro Gly
325 330 335

Val Pro Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg
340 345 350

Thr Glu Arg Phe Gly Gln Gly Ala Gly Pro Val Gly Gly Gln Gly
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35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
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Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Ala Ala Ala Cys
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
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Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
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Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly

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570

575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
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Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
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Lys Phe Asn Lys Val Arg Val Val Arg Ala Leu Asp Ala Val Ala Leu
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Pro Gln Pro Leu Gly Val Pro Asn Glu Ser Gln Ala Leu Ser Gln Arg
660 665 670

Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln Leu Ile Pro Pro Leu Ile
675 680 685

Asn Leu Leu Met Ser Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp
690 695 700

Asn Thr Lys Pro Asp Thr Ser Ser Ser Leu Leu Thr Ser Leu Asn Gln
705 710 715 720

Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu
725 730 735

Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln
740 745 750

Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr
755 760 765

Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu
770 775 780

Asn Glu Gln Arg Met Lys Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr
785 790 795 800

Met Trp Gln Ile Pro Gln Glu Phe Val Lys Leu Gln Val Ser Gln Glu
805 810 815

Glu Phe Leu Cys Met Lys Val Leu Leu Leu Asn Thr Ile Pro Leu
820 825 830

Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr
835 840 845

Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val
850 855 860

Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu
865 870 875 880

His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile
885 890 895

Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val
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Leu Phe His Lys Lys
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35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Ala Ala Ala Val
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
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Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
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Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
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Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
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Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
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Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu

610

615

620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
625 630 635 640

His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
645 650 655

Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
660 665 670

Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Gln Arg Met Lys
675 680 685

Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr Met Trp Gln Ile Pro Gln
690 695 700

Glu Phe Val Lys Leu Gln Val Ser Gln Glu Glu Phe Leu Cys Met Lys
705 710 715 720

Val Leu Leu Leu Leu Asn Thr Ile Pro Leu Glu Gly Leu Arg Ser Gln
725 730 735

Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr Ile Arg Glu Leu Ile Lys
740 745 750

Ala Ile Gly Leu Arg Gln Lys Gly Val Val Ser Ser Ser Gln Arg Phe
755 760 765

Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu His Asp Leu Val Lys Gln
770 775 780

Leu His Leu Tyr Cys Leu Asn Thr Phe Ile Gln Ser Arg Ala Leu Ser
785 790 795 800

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35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
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Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
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Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Val
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
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Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
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Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
625 630 635 640

His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
645 650 655

Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
660 665 670

Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Asp Ser Phe Gly Arg
675 680 685

Ala Thr Lys Ser Asn Pro Val
690 695

<210> 13

<211> 764

<212> PRT

<213> Homo sapiens

<300>

<308> BAC11011

<309> 2004-09-03

<313> (1)..(764)

<400> 13

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Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
Page 31

20

25

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Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
 35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
 50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
 65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
 85 90 95

Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
 100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
 115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
 130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
 145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
 165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
 180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
 195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
 210 215 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
 225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Ala Ala Ala Val
 245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
 260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
 275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Arg Lys Phe Lys Lys Phe Asn Lys Val Arg Val
595 600 605

Val Arg Ala Leu Asp Ala Val Ala Leu Pro Gln Pro Val Gly Val Pro
610 615 620

Asn Glu Ser Gln Ala Leu Ser Gln Arg Phe Thr Phe Ser Pro Gly Gln
625 630 635 640

Asp Ile Gln Leu Ile Pro Pro Leu Ile Asn Leu Leu Met Ser Ile Glu
645 650 655

Pro Asp Val Ile Tyr Ala Gly His Asp Asn Thr Lys Pro Asp Thr Ser
660 665 670

Ser Ser Leu Leu Thr Ser Leu Asn Gln Leu Gly Glu Arg Gln Leu Leu
675 680 685

Ser Val Val Lys Trp Ser Lys Ser Leu Pro Gly Phe Arg Asn Leu His
690 695 700

Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu Met
705 710 715 720

Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln Met
725 730 735

Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Ser His Arg Ser Leu
740 745 750

Ser Ser Phe Lys Leu Ala Lys Lys Ser Ser Ser Val
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<309> 2004-09-03

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35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Gly Gly Gly Ala Ala Ala Val

245

250

255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Phe Arg Asn Leu
625 630 635 640

His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu
645 650 655

Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln
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Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Gln Ser Ile Val
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Thr Ser
690

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Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Gly Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Ala Ala Ala Val
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Ser Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
Page 39

530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
625 630 635 640

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Pro Gln Pro Val Gly Val Pro Asn Glu Ser Gln Ala Leu Ser Gln Arg
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675 680 685

Asn Leu Leu Met Ser Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp
690 695 700

Asn Thr Lys Pro Asp Thr Ser Ser Leu Leu Thr Ser Leu Asn Gln
705 710 715 720

Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu
725 730 735

Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln
740 745 750

Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr
755 760 765

Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu
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Ser Ser Val

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<309> 2004-08-24
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Pro Gly Pro Gly Gly Pro Lys Pro Pro Leu Pro Pro Pro Pro Pro His
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Gln Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln Gln Pro
65 70 75 80

Pro Pro His Gln Gln Pro Pro Pro His Gln Pro Pro His Gln Gln Pro
85 90 95

Pro Pro Pro Pro Gln Glu Ser Lys Pro Val Val Pro Gln Gly Pro Gly
100 105 110

Ser Ala Pro Gly Val Ser Ser Ala Pro Pro Pro Ala Val Ser Ala Pro
115 120 125

Pro Ala Asn Pro Pro Thr Thr Gly Ala Pro Pro Gly Pro Gly Pro Thr
130 135 140

Pro Thr Pro Pro Pro Ala Val Pro Ser Thr Ala Pro Gly Pro Pro Pro
145 150 155 160

Pro Ser Thr Pro Ser Ser Gly Val Ser Thr Thr Pro Pro Gln Thr Gly
165 170 175

Gly Pro Pro Pro Pro Pro Ala Gly Gly Ala Gly Pro Gly Pro Lys Pro
180 185 190

Gly Pro Gly Pro Gly Gly Pro Lys Gly Gly Lys Met Pro Gly Gly Pro
195 200 205

Lys Pro Gly Gly Pro Gly Met Gly Ala Pro Gly Gly His Pro Lys
210 215 220

Pro Pro His Arg Gly Gly Glu Pro Arg Gly Gly Arg Gln His His
225 230 235 240

Ala Pro Tyr His Gln Gln His His Gln Gly Pro Pro Pro Gly Gly Pro
245 250 255

Gly Pro Arg Thr Glu Glu Lys Ile Ser Asp Ser Glu Gly Phe Lys Ala
260 265 270

Asn Leu Ser Leu Leu Arg Arg Pro Gly Glu Lys Thr Tyr Thr Gln Arg
275 280 285

Cys Arg Leu Phe Val Gly Asn Leu Pro Ala Asp Ile Thr Glu Asp Glu
290 295 300

Phe Lys Arg Leu Phe Ala Lys Tyr Gly Glu Pro Gly Glu Val Phe Ile
305 310 315 320

Asn Lys Gly Lys Gly Phe Gly Phe Ile Lys Leu Glu Ser Arg Ala Leu
325 330 335

Ala Glu Ile Ala Lys Ala Glu Leu Asp Asp Thr Pro Met Arg Gly Arg
340 345 350

Gln Leu Arg Val Arg Phe Ala Thr His Ala Ala Ala Leu Ser Val Arg
355 360 365

Asn Leu Ser Pro Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser
370 375 380

Gln Phe Gly Pro Ile Glu Arg Ala Val Val Ile Val Asp Asp Arg Gly
385 390 395 400

Arg Ser Thr Gly Lys Gly Ile Val Glu Phe Ala Ser Lys Pro Ala Ala
405 410 415

Arg Lys Ala Phe Glu Arg Cys Ser Glu Gly Val Phe Leu Leu Thr Thr
420 425 430

Thr Pro Arg Pro Val Ile Val Glu Pro Leu Glu Gln Leu Asp Asp Glu
435 440 445

Asp Gly Leu Pro Glu Lys Leu Ala Gln Lys Asn Pro Met Tyr Gln Lys
450 455 460

Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln His Gly Thr Phe Glu Tyr
465 470 475 480

Glu Tyr Ser Gln Arg Trp Lys Ser Leu Asp Glu Met Glu Lys Gln Gln
485 490 495

Arg Glu Gln Val Glu Lys Asn Met Lys Asp Ala Lys Asp Lys Leu Glu
500 505 510

Ser Glu Met Glu Asp Ala Tyr His Glu His Gln Ala Asn Leu Leu Arg
515 520 525

Gln Asp Leu Met Arg Arg Gln Glu Glu Leu Arg Arg Met Glu Glu Leu
530 535 540

His Ser Gln Glu Met Gln Lys Arg Lys Glu Met Gln Leu Arg Gln Glu
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Glu Glu Arg Arg Arg Glu Glu Glu Met Met Ile Arg Gln Arg Glu
565 570 575

Met Glu Glu Gln Met Arg Arg Gln Arg Glu Glu Ser Tyr Ser Arg Met
580 585 590

Gly Tyr Met Asp Pro Arg Glu Arg Asp Met Arg Met Gly Gly Gly Gly
595 600 605

Thr Met Asn Met Gly Asp Pro Tyr Gly Ser Gly Gly Gln Lys Phe Pro
610 615 620

Pro Leu Gly Gly Gly Ile Gly Tyr Glu Ala Asn Pro Gly Val
625 630 635 640

Pro Pro Ala Thr Met Ser Gly Ser Met Met Gly Ser Asp Met Arg Thr
645 650 655

Glu Arg Phe Gly Gln Gly Ala Gly Pro Val Gly Gly Gln Gly Pro
660 665 670

Arg Gly Met Gly Pro Gly Thr Pro Ala Gly Tyr Gly Arg Gly Arg Glu
675 680 685

Glu Tyr Glu Gly Pro Asn Lys Lys Pro Arg Phe
690 695

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Sequence Listing

SEQ ID NO. 1

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P23246

707 aa linear

Splicing factor, proline-and glutamine-rich (Polypyrimidine tract-binding protein-associated splicing factor) (PTB-associated splicing factor) (PSF) (DNA-binding p52/p100 complex, 100 kDa subunit).

NP_005057

splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens].

15 binding protein associated) [Homo sapiens].

CAA50283

707 aa linear

PTB-associated splicing factor [Homo sapiens].

20

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61 pppphqqqq qpppqpppq qppphqppph pqphqqqqpp pppqdsskpv vaqqpgpapg
121 vgsappasss appatpptsg appgsppgt ptpppavtsa ppgappptpp ssgvpttppq
181 aggpppppaa vpgpgpgpkq gpgrggpkqgg kmpggpkqgg gpglstpgh pkpphrggge
241 prggrqhcpp yhqqhqqgpp pggpggrsee kisdssegfka nlsl1lrpge ktytqrccrlf
301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgrs tgkgivefas
421 kpaarkafer csegvfltt tprpvivepl eqlddedglp eklaqknpmq qkeretpprf
481 aqhgtfeyey sqrwksldem ekqqreqvek nmkdakdkle semedayheh qanllrqdln
541 rrqeelrrme elhnqemqkr kemqlrqeee rrrreeemmi rqremeeqmr xqreesyarm
601 gymdprerdm rmggggamnm gdpygsggqk fpplggggi gyeapgvpp atmmsgsmngs
661 dmrtterfggg gagpvggggp rgmgpgtpag ygrgreeyeg pnkkprf

35 SEQ ID NO. 2

AAH51192

707 aa linear

Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens].

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SEQ ID NO. 3

Isoform short - PSF-F
569aa

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 121 vgsappass appatpptsg appgsgpgpt ptpppavtsa ppgappptp ssgvpttppq
 181 aggpppppaa vpgpgpgpkq gpqpgggpkgg kmpggpkpgg gpglstpgh pkpphrggge
 10 241 prgrqrhhpp yhqqhhqgpp pggpggrsee kisdsegfka nlsllrpge ktytqrclf
 301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
 361 qlrvrfatha aalsvrnlsp yvsnelleea fsqfgpiera vvivddrgrs tgkgivefas
 421 kpaarkafer csegvfltt tprpvivepl eqlddedglp eklaqknpmq qkeretpprf
 481 aqhgtfeyey sgrwksldem ekqqreqvek nmkdakdkle semedayheh qanllrqdln
 15 541 rrqeelrrme elhnqemqkr kemqlrqeee rrrreeemmi rqremeeqmr rqreesysrm
 601 gymdprerdm rmggggamnm gdpygsgqk fpplggggi gyeapgvpp atmmsgsmngs
 661 dmvrmidvg

20 SEQ ID NO. 4

AAH04534
634 aa linear
SFPQ protein [Homo sapiens].

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 121 pgpgpkqgpg pggpkggkmp ggpkpgggpg lstpghpkp phrgggeprg grqhppyhq
 181 qhqqgpppgg pggrseekis dsegfkanls llrrpgekty tqrclfvgn lpaditedef
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 301 svrnlspvys nelleeafsq fgpiereavvi vddrgrstgk givefaskpa arkafercse
 361 gvfltttpr pviveplegl dedglpekl aqknpmqke retpprfaqh gtfeveyesqr
 421 wksldemekq qreqveknmk dakdklesem edayhehgan llrqdlmrrq eelrrmeelh
 481 nqemqkrkem qlrqeerrr reemmirqr emeqmrrqr eesysrmgym dprerdmrmg
 35 541 gggamnmgdp ygsqgqkfpp lgggggigye anpgvppatm sgsmgsmgdmr terfgqggag
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40 SEQ ID NO. 5

AAH27708
525 aa linear
SFPQ protein [Homo sapiens].

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 241 prgrqrhhpp yhqqhhqgpp pggpggrsee kisdsegfka nlsllrpge ktytqrclf
 50 301 vgnlpadite defkrlfaky gepgevfink gkgfgfikle sralaeiaka elddtpmrgr
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 421 kpaarkafer csegvfltt tprpvivepl eqlddedglp eklaqknpmq qkeretpprf
 481 aqhgtfeyey sgrwksldem ekqqreqvek nmkdakdklk kkkkk

SEQ ID. NO. 6

CAA34747

396 aa linear

5 DEFINITION myoblast antigen 24.1D5 (Homo sapiens).

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 121 segvfllttt prpviveple qlldedglpe klagknpmq keretpprfa qhgtfeyey
 181 qrwksldeme kqqreqvekn mdkadkles emedayhehq anllrqdlnr rqeelrrmee
 241 lhngemqkrk emqlrqeeer rrreeemmir qremeeqmrr qreesyarmg ymdprerdmr
 301 mggggammng dpygsggqkf pplggggig yeanpgvppa tmsgsmmgd mrterfgqgg
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15

SEQ ID NO. 7

NM_005066

3071 bp mRNA linear

20 Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA.

X70944 S56626

3071 bp mRNA linear

25 H.sapiens mRNA for PTB-associated splicing factor.

1 ccgccatttt gtgagaagca aggtggcctc cacgtttcct gagcgtcttc ttctgttttg
 61 cctcgaccgc cccttgacca cagacatgtc tcggatcgg ttccggagtc gtggcggtgg
 121 cgggtggc ttccacaggc gtggaggagg cggcggccgc ggccgcctcc acgacttccg
 181 ttctccgcgg cccggcatgg gcctcaatca gaatcgcggc cccatgggtc ctggcccggg
 241 ccagagcggc cctaaggcctc cgatccgc accgcctcca caccaacagc agcaacagcc
 301 accaccgcag cagccaccgc cgcagcagcc gccaccgcatt cagccgcgc cgcattccaca
 361 gccgcattcag cagcagcage cggccgcacc gccgcaggac ttctccaagc ccgtcggtgc
 421 tcagggaccc ggccccgctc ccggagttagg cagcgcacca ccagcttcca gtcggccccc
 481 gcccgcact ccaccaacctt cggggggcccc gccagggtcc gggccaggcc cgactccgac
 541 cccgcgcct gcagtcaccc cggccctcc cggggcgccgc ccacccaccc cgccaaagcag
 601 cgggtccct accacacctc ctcaaggccgg aggccccgcg cctccgcggc cggcagtccc
 661 gggcccggtt ccagggctta agcagggccc aggtccgggt ggtcccaaag gcccggaaaat
 721 gcctggcggtt ccgaagccag gtggcggtttt gggcttaagt acgcctggcg gccaccccaa
 781 gccgcgcattt cgaggcggcg gggagccccc cgggggcgc cagcaccacc cgccctacca
 841 ccagcagcat caccaggggc cccgcgcgg cggggccgc gcgcgcagcg aggagaagat
 901 ctggactcg gaggggttta aagccaattt gtctcttttggcaggaggctg gagagaaaaac
 961 ttacacacag cgatgtcggt tgtttgttgg gaatctacat gctgatataa cggaggatga
 1021 attcaaaaga ctatggata aatatggaga accaggagaa gtttttatca acaaaggcaa
 1081 aggattcgga ttatggatac ttgaatctag agttttggct gaaattgcac aagccgaact
 1141 ggatgataca cccatgagag gttagacatc tcgagttcgc ttgcacac atgctgtgc
 1201 cttttctgtt cgtaatctt caccttatgt ttccatgaa ctgttggaa aagccttttag
 1261 ccaatttgggtt cctattgaaa gggctgtgtt aatagtggat gatcgtggaa gatctacagg
 1321 gaaaggcattt gttgaatttgc cttctaaagcc agcagcaaga aaggcatttgc aacgatgcag
 1381 tgaagggtttt ttcttactga cgacaaactcc tcgtccagtc attgtggaaac cacttgaaca
 1441 actagatgat gaagatggtc ttctgtaaaa acttgcccag aagaatccaa tgtatcaaaa
 1501 ggagagagaa accccttcctc ttgttgcaca gcatggcactt tttgagtagc aatattctca
 1561 gcgatggaaat tctttggatg aaatggaaaa acagcaaagg gaacaagttt gaaaaaaacat
 1621 gaaagatgca aaagacaaat tggaaatgtt aatggaaat gcttatcatg aacatcaggc
 1681 aaatcttttgc cgccaaagatc tgatgagacg acagggagaa ttaagacgca tggaagaact

1741 tcacaatcaa gaaatgcaga aacgtaaaaga aatgcaattt aggcaagagg aggaacgacg
 1801 tagaagagag gaagagatga tgattcgta acgtgagatg gaagaacaaa tgaggcgcca
 1861 aagagaggaa agttacagec gaatgggcta catggatcca cgggaaagag acatgcgaat
 1921 gggtggcgga ggagcaatga acatgggaga tccctatggt tcaggaggcc agaaatttcc
 5 1981 acctcttagga ggtggtggtg gcataggta tgaagcta at cctggcggttc caccagcaac
 2041 catgagtggt tccatgatgg gaagtgcacat gcgtactgag cgctttggc agggaggtgc
 2101 ggggcctgtg ggtggacagg gtccatagg aatggggcct ggaactccag caggatatgg
 2161 tagagggaga gaagagtacg aaggcccgg caaaaaacc cgtatggata tgtgatattt
 2221 aggctttcat tccagttgt ttgttttt ttttagata ccaatctttt aaattcttgc
 10 2281 attttagtaa gaaagctatc ttttatgga tgttagcagt ttattgacat aatatttta
 2341 aatggcttgt tggtggcagg aaaaattatgt aatgcagtgt ttggAACAGG agaattttt
 2401 tttccctttt atttctttt ttttctttt ttactgtata atgtccctca agtttatggc
 2461 agtgtacctr gtgccactga atttccaaag tgtaccaatt tttttttt tactgtgtt
 2521 caaataaata gaaaaatagt tataatattt gatcttcaac tttgccattc atgtttctat
 15 2581 gcatatttgg ctacgtattc cacattgaaa gcatgagat gtctaggcct ttgaatggca
 2641 tatgccattt ctgggaaatg catctggagg ctaagtattt ctttctacaa ataattgccc
 2701 ctttctttt aaaaagaaga aatgcattt gaagtatgtt gatgatgtt tggtcatata
 2761 ggaagcacgc tggtgctaaat tttttttt atggttatgt aagcaaagct gaactgtaaa
 2821 tcttcaggaa tatgtattaa gattgtggaa tgggtgttaa acaattggta ggggggtggaaa
 20 2881 gtgggttga ttaaatggat ctttatggc cctatgatct atcccttact tgaaagctt
 2941 tgaaaagtgg aaaggtcatt ttgtgcatt tccccatttc ttgtttttaa aagaccaaca
 3001 aatctcaagc cctataatg gcttgtattt aacttttaca ttgtatggaa agatgttaaa
 3061 catgaaaaaaaaa a

25

SEQ ID NO. 8

BC051192
 2622 bp mRNA linear
 30 Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated), mRNA (cDNA clone), complete cds.

1 tctgtgtcat ccgccatttt gtgagaagca aggtggcctc cacgtttcct gagcgttttc
 61 ttcgcttttgc cctcgaccgc cccttgcacca cagacatgtc tcgggatcggttccggagtc
 35 121 gtggcggtgg cgggtgggtggc ttccacaggc gtggaggagg cggcgccgc ggcggcctcc
 181 acgacttccg ttctccggcc cccggcatgg gcctcaatca gaatcgccgc cccatgggtc
 241 ctggcccccggc ccagagcgcc cctaaggcctc cgatcccgcc accgcctcca caccaacagc
 301 agcaacagcc accaccgcag cagccaccgc cgeagcagcc gccaccgcat cagccgcgc
 361 cgcattccaca gccgcattcag cagcagcagc cgccgcacc gccgcaggac tcttccaagc
 40 421 ccgtcggtgc tcagggaccc gccccgcgc ccggagttagg cagcacacca ccagcctcca
 481 gctcgcccccc gcccgcact ccaccaacct cggggcccccc gccagggtcc gggccaggcc
 541 cgactccgac cccgcgcct gcagtcacat cggccctcc cggggcgccg ccacccaccc
 601 cgccaaaggcag cggggtcctt accacacccctc ctcaggccgg agggccgcgg cctccgcccc
 661 cggcagtccc gggcccggtt ccagggccta agcagggccc aggtccgggt ggtcccaaag
 45 721 gcgccaaaat gcctggcgcc cccaaaggccag gtggcgcccc gggcctaagt acgcctggcg
 781 gcccacccaa gccgcgcgt cgaggcgccg gggagcccccc cggggccgc cagcaccacc
 841 cgccttacca ccagcagcat caccaggggc cccgcgcgg cggggccgc ggcgcagcg
 901 aggagaagat ctcggactcg gagggtttt aagccaaatgtt ctctcttttgg aggaggctg
 961 gagagaaaaac ttacacacag cgatgtcggt ttgttgcgttgg gaatctacat gctgatatca
 50 1021 cggaggatga attcaaaaaga ctatggata aatatggaga accaggagaa gttttatca
 1081 acaaaggcaa aggattcgga ttatataagc ttgtatctat agctttggct gaaatttgc
 1141 aagccgaact ggtatgataca cccatgagag gtatcagatct tcgatgttcgc tttgccacac
 1201 atgctgtgc cttttctgtt cgtatctt caccttatgt ttccatgaa ctgttggaa
 1261 aagcctttag ccaattttgtt cctattgaaa gggctgttgtt aatagtggat gatcgtggaa
 55 1321 gatctacagg gaaaggcatt gttgaatttgc cttctaaagcc agcagcaaga aaggcatttgc

1381 aacgatgcag tgaagggttt ttcttactga cgacaactcc tcgtccagtc attgtggAAC
 1441 cacttgaaca actagatgtat gaagatggc ttcctgaaaa acgtccccag aagaatccaa
 1501 tgtatcaaaa ggagagagaa accccctactc gtttgccca gcatggcacg tttgagtacg
 1561 aatattctca gcgatggaag tctttggatg aaatggaaaa acagcaaagg gaacaagttg
 5 1621 aaaaaaaaaacat gaaagatgca aaagacaaat tgaaaagtga aatgaaagat gcctatcatg
 1681 aacatcaggc aaatctttg cgccaagatc tgatgagacg acaggaagaa ttaagacgca
 1741 tggagaact tcacaatcaa gaaatgcaga aacgtaaaga aatgcaattt aggcaagagg
 1801 aggaacgacg tagaagagag gaagagatga tgattcgca acgtgagatg gaagaccaaa
 1861 tgaggcgcca aagagaggaa agttacagcc gaatggctt catggatcca cggggaaagag
 10 1921 acatgcgaat ggggtggcgga ggagcaatga acatggaga tccctatggg tcaggaggcc
 1981 agaaatttcc acctcttagga ggtgggtgtg gcataggtt tgaagctaatt cctggcggttc
 2041 caccagcaac catgagttgtt tccatgtatgg gaagtgcacat gcgtactgag cgcttgggc
 2101 agggaggtgc ggggcctgtg ggtggacagg gtcctagagg aatggggcctt ggaactccag
 2161 caggatatgg tagagggaga gaagagtacg aaggcccaaa caaaaaaccc cgattttaga
 15 2221 tgttatattt aggcttcatt tccagttgtt ttgtttttt tgtttagata ccaatctttt
 2281 aaattcttgc attttagtaa gaaagctatc ttttatgg ttttagcagt ttattgacct
 2341 aatatttgc aatggctgtt ttggcaggt aaaattatgt aatgcagtgt ttggAACAGG
 2401 agaattttttt ttccctttt attctttat ttttctttt ttactgtata atgtccctca
 2461 agtttatggc agtgtacctt gtgccactga attccaaag tgtaccaattt tttttttttt
 20 2521 tactgtgctt caaataaata gaaaaatagt tataaaaaaaa aaaaaaaaaaa aaaaaaaaaaa
 2581 aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aa

SEQ ID NO. 9

25

X16850.

2021 bp mRNA linear

Human mRNA for myoblast cell surface antigen 24.1D5.

30 1 gaattcaaaa gactatttgc taaatatggaa gaaccaggag aagttttat caacaaaggc
 61 aaaggattcg gatttattaa gcttgaatct agagcttgg ctgaaattgc caaagccgaa
 121 ctggatgata cacccatgag aggttagacag cttcgagtcc gcttgcac acatgctgct
 181 gccccttctg ttcgtaatct ttcacctt gttccaatg aactgttgg aagaagcctt
 241 agccaaatttgc gtcctatttga aagggtgtt gtaatagtgg atgatcggtt aagatctaca
 301 gggaaaggca ttgttgaatt tgcttctaag ccagcagcaa gaaaggcatt tgaacgatgc
 361 agtgaaggtg ttttcttact gacgacaact cctcgccatc tcattgtgg accacttggaa
 421 caacttagatg atgaagatgg ttttccttgc aaacttgccc agaagaatcc aatgtatcaa
 481 aaggagagag aaaccctcc tcgttttgc cagcatggca cgtttgagta cgaatattct
 541 cagcgatggc agtcttgg taaaatggaa aaacagcaa gggaaacaatg taaaaaaac
 40 601 atgaaagatg caaaagacaa attggaaatg gaaatggaaatg atgcctatca tgaacatcg
 661 gcaaattttt tgcgc当地 aactgttggaa cggcaggaaatg aattaagacg catggaaagaa
 721 cttcacaatc aagaaatgc gaaacgtaaa gaaatgcatt tgaggcaaga ggaggAACGA
 781 cgtagaagag aggaagagat gatgattcgtaa acgttgcata tggaaaca aatgaggcgc
 841 caaagagagg aaagttacag ccgaatggc tacatggatc cacggaaatg agacatgcga
 45 901 atgggtggcg gaggagcaat gaaatggaa gatccctatg gttcaggagg ccagaaattt
 961 ccacctctatc gaggtgggtgg tggcataggt tatgaagcta atcctggcg tccaccagca
 1021 accatgagtg gttccatgtat gggaaatgtac atgcgtactg agcgcttgg gcaggaggat
 1081 gcggggcctg tgggtggaca gggctctaga gaaatggggc ctggaaatcc agcaggatatt
 1141 ggttagagggaa gagaagatg cgaaggccca aacaaaaaaac cccgattttt gatgtatatt
 50 1201 ttaggctttc attccagttt gttttgtttt tttgtttaga tccaaatctt taaaattttt
 1261 gcattttatgtt aagaaagctt tctttttatg gatgttagca gtttattgac ctaatatttg
 1321 taaatggctt gtttggcag gtaaaattat gtaatgcagt gtttggaaaca ggagaatttt
 1381 ttttccctttt tatttcttta ttttttcttt tttactgtat aatgtccctc aagtttatgg
 1441 cagtgtacct tggccactg aattccaaat gtttgcacat tttttttttt ttactgtgt
 55 1501 tcaaataat agaaaaatag ttataatattt gatcttcaac tttggccatcc atgcttctat

1561 gcatattagg ctacgttattc cacattgaaa gcatgagagt gtctaggcct ttgaatggca
1621 tatgccattt ctgggaaatg catctggagg ctaagtattt ctttctacaa ataattgccc
1681 cctttttttt aaaaagaaga aatgcattt gaagtagttt gatgatttgt ttggcatata
1741 ggaagcacgc tggtgctaag tatttttaa atggttatgt aagcaaagct gaactgtaaa
1801 tcttcaggaa tatgtattaa gattgtggaa tgggtgttaag acaattggta ggggtgaaa
1861 gtgggtttga ttaaatggat cttttatgac cctatgatct atcccttact tgaaagctt
1921 tgaaaagtgg aaaggtcatt ttgttgattt ccocccatttc ttgttttaa aagaccaaca
1981 aatctcaagc cctataaatg gcttgtattt aacccgaatt c

10

SEQ ID NO. 10

NP_000917

933 aa linear

15

progesterone receptor [Homo sapiens]

AAS00096

933 aa linear

progesterone receptor [Homo sapiens]

20

AAD01587

933 aa linear

progesterone receptor [Homo sapiens]

25

AAA60081

933 aa linear

progesterone receptor Homo sapiens

P06401

30

933 aa linear

Progesterone receptor (PR).

1 mtelkakgpr aphvaggpps pevgspillcr paagpfpgsq tsdtlpevs ipisldgllf
61 prpcqgqdps dektqdqqsl sdvegaysra eatrgagss ssppekdsgl ldsvltdlla
35 121 psgpgqqsqps ppacettsrw clfgpelped ppaapatqrv lsplm srsgc vgdssgtaa
181 ahkvlprglr parqlllpas esphwsgapv kpspqaaave veeedssese esagpllkkgk
241 pralggaaag ggaaacppga aaggvalvpk edsrfsaprv alveqdapma pgrsplattv
301 mdfihvpilp lnhallart rqlledesyd ggagaasafa pprtspcass tpvavgdfpd
361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
40 421 pppplpprat psrpgeaavt aapasavss asssgstlec ilykaegapp qqgpfaapppc
481 kapgasgcil prdglpstsa saaaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrpdsse asqspqysfe slpkiclic gdeasgchyg vltcgscckvf fkrameeqhn
601 ylcagrndci vdkirrkncp acrlrkccqa gmvlgrkfk kfnkvrvvra ldavalpqpl
661 gvpnesqals qrftfsgqod iqlipplnl lmsiepdviy aghdntkpdt ssslltslnq
721 lgerqlsrrv kwskslpgfr nlhiddqitl iqyswmslmv fglgwrsykh vsgqmlyfap
781 dlilneqrmk essfyslclt mwqipqefvk lqvsqeeflc mkvllllnti pleglrsqtq
841 feemrssyir elikaiglrq kgvvssssqrf yqltklldnl hdlvkqlhly clntfiqsra
901 lsvefpeemm eviaaqlpki lagmvkpllf hkk

50

SEQ ID NO. 11

BAB91074

831 aa linear

55

delta 4 progesterone receptor [Homo sapiens]

1 mtelkakgpr aphvaggpps pevgsplicr paagpfpgsq tsdtlpevs ipisldgllf
 61 prpcqggdps dektqdqqsl sdvegaysra eatrgaggss sspekdsgl ldsvltdlla
 121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
 181 ahkvlpgrls parql1pas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
 241 pralggaaag ggaaavppga aaggvalvpk edsrfapsrv alveqdapma pgrsplattv
 301 mdfihvpilp lnhaltaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
 421 pppplpprat psrpgeaavt aapatasvss assgstlec ilykaegapp qqgpffappc
 481 kapgasgcll prdglpstsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
 541 ylnylrpds asqspqysfe slpkiclic gdeasgchyg vltcgsckvf fkramegqhn
 601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrnl hiddqitliq yswmslmvfg
 661 lgwrsykhvs gqmlyfadpl ilneqrmkf sfyslcltmw qipqefvklq vsqeeflcmk
 721 vllllntipl eglrsqtqfe emrssyirel ikaiglrqkg vvsssqrfyq ltklldnlhd
 781 lvkqlhlycl ntfiqsrals vefpemmsev iaqlpkila gmvkpllfhk k

SEQ ID NO. 12

BAC06585
 20 695 aa linear
 Progesterone receptor [Homo sapiens]

1 mtelkakgpr aphvaggpps pevgsplicr paagpfpgsq tsdtlpevs ipisldgllf
 61 prpcqggdps dektqdqqsl sdvegaysra eatrgaggss sspekdsgl ldsvltdlla
 121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
 181 ahkvlpgrls parql1pas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
 241 pralggaaag ggaaavppga aaggvalvpk edsrfapsrv alveqdapma pgrsplattv
 301 mdfihvpilp lnhaltaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
 421 pppplpprat psrpgeaavt aapatasvss assgstlec ilykaegapp qqgpffappc
 481 kapgasgcll prdglpstsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
 541 ylnylrpds asqspqysfe slpkiclic gdeasgchyg vltcgsckvf fkramegqhn
 601 ylcagrndci vdkirrkncp acrlrkccqa gmvlggfrnl hiddqitliq yswmslmvfg
 661 lgwrsykhvs gqmlyfadpl ilndsfgrat knp

35

SEQ ID NO. 13

BAC11011
 40 764 aa linear
 delta 3+6/2 progesterone receptor [Homo sapiens].

1 mtelkakgpr aphvaggpps pevgsplicr paagpfpgsq tsdtlpevs ipisldgllf
 61 prpcqggdps dektqdqqsl sdvegaysra eatrgaggss sspekdsgl ldsvltdlla
 121 psgpgqsqps ppacevtssw clfgpelped ppaapatqrv lsplmsrsgc kvgdssgtaa
 181 ahkvlpgrls parql1pas esphwsgapv kpspqaaave veeedgsese esagpllkkgk
 241 pralggaaag ggaaavppga aaggvalvpk edsrfapsrv alveqdapma pgrsplattv
 301 mdfihvpilp lnhaltaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
 421 pppplpprat psrpgeaavt aapatasvss assgstlec ilykaegapp qqgpffappc
 481 kapgasgcll prdglpstsa saaaagaapa lypalglngl pqlgyqaavl keglpqvypp
 541 ylnylrpds asqspqysfe slpkiclic gdeasgchyg vltcgsckvf fkamegrkf
 601 kkfnkvrvvrr aldavalpqp vgvpnesqal sgrftfsgq diglipplin llmsiepdvi
 661 yaghdnktkd tsssltsln qlgerqlsv vkwskslpgf rnlihiddqit liqyswmelm
 721 vfglgwrsyk hvsgqmlfy pdlilnashr slssfkakk sssv

SEQ ID NO.14

5 BAC11012
690 aa linear
delta4+6/2 progesterone receptor [Homo sapiens]

10 1 mtelkakgpr aphvaggpp s pevgsp llcr paagpfpgsq tsdtlpevsa ipisldgllf
61 prpcqgq dps dektqdqqsl sdvegaysra eatrgaggss ssppekds gl lds vldtlla
121 psgpgq sqps pp acevtssw clfgpelped ppaap atqrv lsplmsrsgc kvgdssgtaa
181 ahkvlp rgl s parql lpa s esphwsgapv kp spqaa ave veeedgsese esagpl lk gk
241 pralggaa ag ggaaavppga aaggvalvpk eds rfsap rv alveq dapma pgrsplattv
301 mdfihvpilp ln hallaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
15 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aap asasvss ass gstlec ilykaegapp qqgpfa appc
481 kapgasgc l1 prdglp stsa saaaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrp dse asqspqysfe slpkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccq a gmvlggfrnl hiddqitliq ys wmsl mvfg
20 661 lgwrsykh vs qmlyfap dl ilneqsivts

SEQ ID NO.15

25 BAC11013
803 aa linear
delta 6/2 progesterone receptor [Homo sapiens].

30 1 mtelkakgpr aphvaggpp s pevgsp llcr paagpfpgsq tsdtlpevsa ipisldgllf
61 prpcqgq dps dektqdqqsl sdvegaysra eatrgaggss ssppekds gl lds vldtlla
121 psgpgq sqps pp acevtssw clfgpelped ppaap atqrv lsplmsrsgc kvgdssgtaa
181 ahkvlp rgl s parql lpa s esphwsgapv kp spqaa ave veeedgsese esagpl lk gk
241 pralggaa ag ggaaavppga aaggvalvpk eds rfsap rv alveq dapma pgrsplattv
301 mdfihvpilp ln hallaart rqlledesyd ggagaasafa pprsspcass tpvavgdfpd
35 361 cayppdaepk ddayplysdf qppalkikee eegaeasars prsylvagan paafpdfplg
421 pppplpprat psrpgeaavt aap asasvss ass gstlec ilykaegapp qqgpfa appc
481 kapgasgc l1 prdglp stsa saaaaagaapa lypalglngl pqlgyqaavl keglpqvypp
541 ylnylrp dse asqspqysfe slpkiclic gdeasgchyg vltcgsckvf fkramegqhn
601 ylcagrndci vdkirrkncp acrlrkccq a gmvlggfrnl kfnkvrvvra lda valpqp v
40 661 gvpnesqals qrftf spgqd iq lipplnl lmsiepdviy aghdntkpdt ssslltslnq
721 lgerql lsvv kwks lpgfr nlhiddqitl iq yswmsl mv fglgwrsykh vsgqmlyfap
781 dlilneshrs lssfkla kks ssv

45 SEQ ID NO. 16

FGQGGAGPVGGQGP

50 SEQ ID NO.17

CTGAGTC

55 SEQ ID NO. 18

YGEPEVFINKKGK

5 SEQ ID NO. 19

GIVEFASKPAAR

10 SEQ ID NO. 20

FAQHGTEEYEYSQR

15 SEQ ID NO. 21

NP_076092 (Murine PSF)

20 1 msrdrfrsrg gggggfhrrg ggggrggld frspppgmgl nqnrppmgpg pggpkppplpp
61 pphhqqqqqp ppqqpppqpp pphhqqppphq pphhqqppppp qeskpvvpqg pgsapgvssa
121 pppavsaapp nppttgappg pgptptpppa vpstapgppp pstpssgvst tppqtggppp
181 ppaggagpgp kpgpgpggpk ggkmpggpkp gggpgmgapg ghpkpphrgg geprggrqhh
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SEQ ID NO. 22

35 VRMIDVG